

Result No.	Score	Query Match	Length	DB	ID	Description
1	615	100.0	766	12	US-10-664-456-12	Sequence 12, Appl
2	615	100.0	787	12	US-10-664-456-13	Sequence 13, Appl
3	615	100.0	820	12	US-10-664-456-14	Sequence 14, Appl
4	615	100.0	820	16	US-10-408-765A-1252	Sequence 1252, Ap
5	557	90.6	528	9	US-09-792-200B-22	Sequence 22, Appl
6	446	72.5	726	12	US-10-633-202-2	Sequence 2, Appl
7	446	72.5	726	14	US-10-456-028-3	Sequence 3, Appl
8	446	72.5	776	10	US-09-978-418-6	Sequence 6, Appl
9	443	72.0	722	14	US-10-265-125-2	Sequence 2, Appl
10	443	72.0	722	15	US-10-074-978A-288	Sequence 288, App
11	443	72.0	722	15	US-10-074-978A-289	Sequence 289, App
12	431	70.1	446	9	US-09-792-200B-12	Sequence 12, Appl
13	431	70.1	535	12	US-10-633-202-3	Sequence 3, Appl
14	422	68.6	523	9	US-09-792-200B-14	Sequence 14, Appl
15	408	66.3	729	15	US-10-074-978A-287	Sequence 287, App

```

RESULT 2
US-10-664-456-13
; Sequence 13, Application US/10664456
; Publication No. US20040038364A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; TITLE OF INVENTION: NEW METALLOPROTEINASE-DISINTEGRIN FAMILY MEMBERS: SVPH
; TITLE OF INVENTION: DNAS AND POLYPEPTIDES
; FILE REFERENCE: 03260.0093-00304
; CURRENT APPLICATION NUMBER: US/10/664,456
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: prior APPLICATION NUMBER: US/09/890,323
; PRIOR FILING DATE: prior FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/116,670
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 60/138,682
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: 60/155,798
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-456-13

Query Match 100.0%; Score 615; DB 12; Length 787;
Best Local Similarity 100.0%; Pred. No. 4.4e-49;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHTKDIENVKRCGVVEEGECDCGPKLHKCAKDPCCLSNCTLTGSGTCAFLGCKCKCKF 60
Db 389 VHTKDIENVKRCGVVEEGECDCGPKLHKCAKDPCCLSNCTLTGSGTCAFLGCKCKCKF 448

Qy 61 LPSGKVCRCKEVNECDLPWCNGTSHKCPDDFYVEDGIPCKERG 103
Db 449 LPSGKVCRCKEVNECDLPWCNGTSHKCPDDFYVEDGIPCKERG 491

RESULT 3
US-10-664-456-14
; Sequence 14, Application US/10664456
; Publication No. US20040038364A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; TITLE OF INVENTION: NEW METALLOPROTEINASE-DISINTEGRIN FAMILY MEMBERS: SVPH
; TITLE OF INVENTION: DNAS AND POLYPEPTIDES
; FILE REFERENCE: 03260.0093-00304
; CURRENT APPLICATION NUMBER: US/10/664,456
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: prior APPLICATION NUMBER: US/09/890,323
; PRIOR FILING DATE: prior FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/116,670
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 60/138,682
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: 60/155,798
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-456-14

Query Match 100.0%; Score 615; DB 12; Length 820;
Best Local Similarity 100.0%; Pred. No. 4.4e-49;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHTKDIENVKRCGVVEEGECDCGPKLHKCAKDPCCLSNCTLTGSGTCAFLGCKCKCKF 60
Db 389 VHTKDIENVKRCGVVEEGECDCGPKLHKCAKDPCCLSNCTLTGSGTCAFLGCKCKCKF 448

Qy 61 LPSGKVCRCKEVNECDLPWCNGTSHKCPDDFYVEDGIPCKERG 103
Db 449 LPSGKVCRCKEVNECDLPWCNGTSHKCPDDFYVEDGIPCKERG 491

RESULT 4
US-10-408-765A-1252
; Sequence 1252, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1252
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1252

Query Match 100.0%; Score 615; DB 16; Length 820;
Best Local Similarity 100.0%; Pred. No. 4.6e-49;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHTKDIENVKRCGVVEEGECDCGPKLHKCAKDPCCLSNCTLTGSGTCAFLGCKCKCKF 60
Db 389 VHTKDIENVKRCGVVEEGECDCGPKLHKCAKDPCCLSNCTLTGSGTCAFLGCKCKCKF 448

Qy 61 LPSGKVCRCKEVNECDLPWCNGTSHKCPDDFYVEDGIPCKERG 103
Db 449 LPSGKVCRCKEVNECDLPWCNGTSHKCPDDFYVEDGIPCKERG 491

RESULT 5
US-09-792-200B-22
; Sequence 22, Application US/09792200B
; Patent No. US20020042368A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Fanslow, William C.
; APPLICANT: Poindexter, Kurt
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Black, Roy A.
; TITLE OF INVENTION: INTEGRIN ANTAGONISTS
; FILE REFERENCE: 2958-A
; CURRENT APPLICATION NUMBER: US/09/792,200B
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/184,865
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion Construct
US-09-792-200B-22
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2004, 22:00:41 ; Search time 123 Seconds  
(without alignments)  
236.605 Million cell updates/sec

Title: US-10-664-456-12\_COPY\_389\_491

Perfect score: 615

Sequence: 1 VHTKIDIFNVKRCGVVEG.....SHKCPDDFYVEDGIPCKERG 103

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	615	100.0	766	3	AAB07739	Aab07739 A snake v
2	615	100.0	787	3	AAB07740	Aab07740 A snake v
3	615	100.0	820	3	AAB07741	Aab07741 A snake v
4	557	90.6	528	4	AAE13061	Aae13061 ADAM-29di
5	446	72.5	726	2	AAE17413	Aae17413 Human SVP
6	446	72.5	726	2	AAE17413	Aae17413 Human SVP
7	446	72.5	726	7	ADC78877	Adc78877 Human PRO
8	446	72.5	776	6	ABR39425	Abc39425 Human GEN
9	443	72.0	542	2	AAE13061	Aae13061 ADAM-26
10	443	72.0	722	2	AAE13061	Aae13061 ADAM-26
11	443	72.0	722	6	ABG76200	Abg76200 Human sna
12	431	70.1	535	2	AAE17414	Aae17414 SVPHI-26
13	431	70.1	535	4	AAE13056	Aae13056 ADAM-21di
14	422	68.6	523	4	AAE13057	Aae13057 ADAM-21di
15	357	58.0	499	3	AAB07738	Aab07738 A snake v
16	357	58.0	781	3	AAB07743	Aab07743 A snake v
17	357	58.0	790	3	AAB07742	Aab07742 A snake v
18	357	58.0	790	3	AAB07705	Aab07705 Amino aci
19	357	58.0	790	4	AAU12273	Aau12273 Human PRO
20	357	58.0	790	6	ABO17717	Abol17717 Novel hum
21	357	58.0	790	6	ABU80971	Abu80971 Human PRO
22	357	58.0	790	6	ABU66671	Abu66671 Human PRO
23	357	58.0	790	6	ABU59752	Abu59752 Novel sec
24	357	58.0	790	6	ABO24942	Abol24942 Human sec
25	357	58.0	790	6	ABU66947	Abu66947 Human sec

ALIGNMENTS

RESULT 1

AAB07739  
ID AAB07739 standard; protein; 766 AA.

XX AAB07739;

AC AAB07739;

XX 07-NOV-2000 (first entry)

DT 07-NOV-2000 (first entry)

DE A snake venom protease (SVPH-1) polypeptide varaint SVPH-1a.

XX Snake venom protease; SVPH; SVPH-1; metalloproteinase-disintegrin;

KW chromosome 1; chromosome 4; immune system; splice variant.

OS Homo sapiens.

XX WO2000043525-A2.

PN WO2000043525-A2.

XX 27-JUL-2000.

PD 21-JAN-1999; 2000WO-US001338.

PF 21-JAN-1999; 99US-0116670P.

PR 14-JUN-1999; 99US-0138682P.

PR 27-SEP-1999; 99US-0155798P.

XX (IMMV ) IMMUNEX CORP.

PI Cerretti DP;

XX WPI; 2000-482914/42.

DR N-ESDB; AAA59304.

XX Snake venom protease (SVPH) nucleic acids, and polypeptides, used to

PT identify proteins having metalloproteinase-disintegrin activity, and

PT inhibitors of the proteins for use in therapeutics.

XX Claim 13; Page 15; 105pp; English.

CC The present sequence represents an alternatively spliced snake venom

CC protease-1 (SVPH-1) polypeptide, designated SVPH-1a. The SVPH

CC polypeptides are metalloproteinase-disintegrin protein family members.

CC The SVPH polynucleotides can be used as probes to identify nucleic acids

CC encoding proteins having metalloproteinase-disintegrin activity, to

CC identify human chromosome 1 or 4, to map genes on those chromosomes, to

CC identify genes associated with diseases, syndromes and conditions

CC associated with the chromosomes, and to study proteinases and their

CC activities on cell/cell interactions and the immune system. Sense or

CC antisense oligonucleotides of SVPH can be used to inhibit gene expression

CC of SVPH 1, 3, or 4. The SVPH polypeptides can be used to study cell/cell  
CC and cell/matrix interactions involved in cellular processes and in the  
CC immune system. The polypeptides may also be used to screen for inhibitors  
CC of the polypeptide's activity, which are used in therapeutics. The  
CC antibodies can be used in assays to detect the presence of the  
CC polypeptides in vitro or in vivo, and to purify the polypeptides by  
CC affinity chromatography  
XX  
SQ Sequence 766 AA;

Query Match 100.0%; Score 615; DB 3; Length 766;  
Best Local Similarity 100.0%; Pred. No. 6.9e-43;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VHTKDI FNVKRCGVVEEGECDCGPKLKHCAKDPCCLSNCTLTLDGSTCAFLGCKCKCF 60  
Db 389 VHTKDI FNVKRCGVVEEGECDCGPKLKHCAKDPCCLSNCTLTLDGSTCAFLGCKCKCF 448  
Qy 61 LPSGKVC RKEVNECDLPWCNGTSHKCPDDPFYVDGIPCKERG 103  
Db 449 LPSGKVC RKEVNECDLPWCNGTSHKCPDDPFYVDGIPCKERG 491

RESULT 2  
AAB07740  
ID AAB07740 standard; protein; 787 AA.  
XX  
AC AAB07740;  
XX  
DT 07-NOV-2000 (first entry)  
XX  
DE A snake venom protease (SVPH-1) polypeptide variant SVPH-1b.  
XX  
KW Snake venom protease; SVPH; SVPH-1; metalloproteinase-disintegrin;  
KW chromosome 1; chromosome 4; immune system; splice variant.  
XX  
OS Homo sapiens.

XX WO200043525-A2.  
XX 27-JUL-2000.  
XX 21-JAN-2000; 2000WO-US001338.  
XX 21-JAN-1999; 99US-0116670P.  
PR 14-JUN-1999; 99US-0138682P.  
PR 27-SEP-1999; 99US-0155798P.  
XX  
XX (IMMV ) IMMUNEX CORP.  
XX  
XX Cerretti DP;  
XX WPI; 2000-482914/42.  
DR N-ESDB; AAA59305.  
XX  
XX Snake venom protease (SVPH) nucleic acids, and polypeptides, used to  
PT identify proteins having metalloproteinase-disintegrin activity, and  
PT inhibitors of the proteins for use in therapeutics.  
XX  
XX Claim 13; Page 15-16; 105pp; English.

XX The present sequence represents an alternatively spliced snake venom  
CC protease-1 (SVPH-1) polypeptide, designated SVPH-1b. The SVPH  
CC polypeptides are metalloproteinase-disintegrin protein family members.  
CC The SVPH polynucleotides can be used as probes to identify nucleic acids  
CC encoding proteins having metalloproteinase-disintegrin activity, to  
CC identify human chromosome 1 or 4, to map genes on those chromosomes, to  
CC identify genes associated with diseases, syndromes and conditions  
CC associated with the chromosomes, and to study proteinases and their  
CC activities on cell/cell interactions and the immune system. Sense or  
CC antisense oligonucleotides of SVPH can be used to inhibit gene expression  
CC of SVPH 1, 3, or 4. The SVPH polypeptides can be used to study cell/cell  
CC and cell/matrix interactions involved in cellular processes and in the

CC immune system. The polypeptides may also be used to screen for inhibitors  
CC of the polypeptide's activity, which are used in therapeutics. The  
CC antibodies can be used in assays to detect the presence of the  
CC polypeptides in vitro or in vivo, and to purify the polypeptides by  
CC affinity chromatography  
XX  
SQ Sequence 787 AA;

Query Match 100.0%; Score 615; DB 3; Length 787;  
Best Local Similarity 100.0%; Pred. No. 7.1e-43;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VHTKDI FNVKRCGVVEEGECDCGPKLKHCAKDPCCLSNCTLTLDGSTCAFLGCKCKCF 60  
Db 389 VHTKDI FNVKRCGVVEEGECDCGPKLKHCAKDPCCLSNCTLTLDGSTCAFLGCKCKCF 448  
Qy 61 LPSGKVC RKEVNECDLPWCNGTSHKCPDDPFYVDGIPCKERG 103  
Db 449 LPSGKVC RKEVNECDLPWCNGTSHKCPDDPFYVDGIPCKERG 491

RESULT 3  
AAB07741  
ID AAB07741 standard; protein; 820 AA.  
XX  
AC AAB07741;  
XX  
DT 07-NOV-2000 (first entry)  
XX  
DE A snake venom protease (SVPH-1) polypeptide variant SVPH-1c.  
XX  
KW Snake venom protease; SVPH; SVPH-1; metalloproteinase-disintegrin;  
KW chromosome 1; chromosome 4; immune system; splice variant.  
XX  
OS Homo sapiens.

XX WO200043525-A2.  
XX 27-JUL-2000.  
XX 21-JAN-2000; 2000WO-US001338.  
XX 21-JAN-1999; 99US-0116670P.  
PR 14-JUN-1999; 99US-0138682P.  
PR 27-SEP-1999; 99US-0155798P.  
XX  
XX (IMMV ) IMMUNEX CORP.  
XX  
XX Cerretti DP;  
XX WPI; 2000-482914/42.  
DR N-ESDB; AAA59306.  
XX  
XX Snake venom protease (SVPH) nucleic acids, and polypeptides, used to  
PT identify proteins having metalloproteinase-disintegrin activity, and  
PT inhibitors of the proteins for use in therapeutics.  
XX  
XX Claim 13; Page 16; 105pp; English.

XX The present sequence represents an alternatively spliced snake venom  
CC protease-1 (SVPH-1) polypeptide, designated SVPH-1c. The SVPH  
CC polypeptides are metalloproteinase-disintegrin protein family members.  
CC The SVPH polynucleotides can be used as probes to identify nucleic acids  
CC encoding proteins having metalloproteinase-disintegrin activity, to  
CC identify human chromosome 1 or 4, to map genes on those chromosomes, to  
CC identify genes associated with diseases, syndromes and conditions  
CC associated with the chromosomes, and to study proteinases and their  
CC activities on cell/cell interactions and the immune system. Sense or  
CC antisense oligonucleotides of SVPH can be used to inhibit gene expression  
CC of SVPH 1, 3, or 4. The SVPH polypeptides can be used to study cell/cell  
CC and cell/matrix interactions involved in cellular processes and in the  
CC immune system. The polypeptides may also be used to screen for inhibitors  
CC of the polypeptide's activity, which are used in therapeutics. The

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 27, 2004, 22:09:37 ; Search time 39 Seconds  
(without alignments)  
254.044 Million cell updates/sec

Title: US-10-664-456-12\_COPY\_389\_491  
Perfect score: 615  
Sequence: 1 VHTKDIPNVKRCGVVVEG.....SHKCPDDFYVEDGIPCKERG 103

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	314	51.1	473	2	I49283
2	306.5	49.8	655	2	JC7850
3	306.5	49.8	660	2	S71949
4	305.5	49.7	732	2	I52361
5	294	47.8	903	2	S60257
6	293	47.6	713	2	I65253
7	289	47.0	735	2	I48101
8	282	45.9	825	2	S55060
9	282	45.9	905	2	S55059
10	266	43.3	600	2	I49281
11	263.5	42.8	734	2	JC4861
12	262	42.6	617	2	S48160
13	261	42.4	357	2	S23403
14	261	42.4	524	2	S38539
15	261	42.4	670	2	I65967
16	260.5	42.4	735	2	G02937
17	259	42.1	150	2	S60258
18	257	41.8	776	2	S28258
19	256	41.6	826	2	A60395
20	253	41.1	789	2	S28259
21	251.5	40.9	429	2	A42972
22	251	40.8	571	2	S24789
23	251	40.8	609	2	S55270
24	250.5	40.7	512	2	T37819
25	249.5	40.6	952	2	T18900
26	249	40.5	419	2	A59414
27	245.5	39.9	814	2	G02390
28	244.5	39.8	756	2	S47656
29	241.5	39.3	151	2	S60259

30 240.5 39.1 610 2 JC7530 vascular apoptosis  
31 240 39.0 419 2 S41607 atrolysin A (EC 3.  
32 232 37.7 549 2 S481609 metalloproteinase  
33 230.5 37.5 777 2 I48100 ADAM 5 protein pre  
34 229 37.2 216 2 JX0265 platelet aggregati  
35 229 37.2 616 2 A55796 ecarin precursor -  
36 227 36.9 416 2 A37877 hemorrhagic protei  
37 218.5 35.5 736 2 S47645 tMDC I protein - c  
38 218.5 35.5 823 2 S18968 cyritestin precurs  
39 215.5 35.0 1042 2 T26644 hypothetical prote  
40 212 34.5 209 2 JX0266 platelet aggregati  
41 191.5 31.1 83 2 F35982 bitan alpha - puff  
42 183.5 29.8 83 2 A34156 bitistatin - puff  
43 181 29.4 480 1 A30065 trigramin precurs  
44 180.5 29.3 71 2 A33990 aploggin - easter  
45 178 28.9 71 2 A59409 platelet-aggregati

ALIGNMENTS

RESULT 1  
I49283  
ADAM 4 protein precursor - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 03-Nov-2000  
C:Accession: I49283  
R:Wolfsberg, T.G.; Straight, P.D.; Gerena, R.L.; Huovila, A.P.; Primakoff, P.; Myles, D.  
Dev. Biol. 169, 378-383, 1995  
A>Title: ADAM, a widely distributed and developmentally regulated gene family encoding m  
A:Reference number: I48100; MUID:95269891; PMID:7750654  
A:Accession: I49283  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-473 <RES>  
A:Cross-references: EMBL:U20508; NID:965013; PIDN:AAA74922.1; PID:965014  
C:Genetics:  
A:Gene: ADAM4  
C:Superfamily: mouse meltrin alpha; disintegrin homology  
F:129-211/Domain: disintegrin homology <DIS>

Query Match 51.1%; Score 314; DB 2; Length 473;  
Best Local Similarity 52.6%; Pred. No. 1.7e-19;  
Matches 50; Conservative 13; Mismatches 32; Indels 0; Gaps 0;

Qy 5 DIPNVKRCGVVVEGEECCGPKLHKCAKDPCCLSNCTLTDTGSTCAFGCLCKCKCKFLPSG 64  
Db 126 NMVEVPCGNKRVASEKDCGSGVKDCTTKCCVNCFEFTQGSSCAAGGCLCKCKFAPTG 185  
Qy 65 KVCRCYNECDLPEWCNGTSHKCPDDFYVEDGIPC 99  
Db 186 TICRDKNGICDLPYCSGSEHCFCGNFYIMDGTTC 220

RESULT 2  
JC7850  
disintegrin and metalloproteinase(ADAM) 9 protein, short form - human  
N:Alternate names: MDC9 protein; meltrin gamma  
C:Species: Homo sapiens (man)  
C>Date: 18-Nov-2002 #sequence\_revision 18-Nov-2002 #text\_change 31-Mar-2003  
C:Accession: JC7850  
R:Hotoda, N.; Koike, H.; Sasaagawa, N.; Ishiura, S.  
Biochem. Biophys. Res. Commun. 293, 800-805, 2002  
A>Title: A secreted form of human ADAM9 has an alpha-secretase activity for APP.  
A:Reference number: JC7850; MUID:22050095; PMID:12054541  
A:Accession: JC7850  
A:Molecule type: mRNA  
A:Residues: 1-655 <HOT>  
A:Cross-references: GB:AF495383  
C:Comment: This protein, which is a member of the a disintegrin and metalloprotease (ADA  
lular functions. It is proteolytically active, and has an alpha-secretase activity for a  
C:Genetics:  
A:Gene: adam9s

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Query Match      49.8%; Score 306.5; DB 2; Length 655;
Best Local Similarity 49.5%; Pred. No. 9.4e-19;
Matches 48; Conservative 19; Mismatches 29; Indels 1; Gaps 1;

Qy 5 DIFNVKRCNGVVEGEECDGGLPKHKCAKDPCLL-SNCTLTGSGTCAFGLCCKDKCKFLPS 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 410 EAYSAPSGCNKLVDAAGECDGCTPKCELDPCCGSGTCKLSPFAECAYGDCCKDCRFLPG 469
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 64 GKVKRKEVNECDLPEWNCNGTSHKCPDDPFYVBDGIPCK 100
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 470 GTLCRGKTSECDVPCYCNSSQFCQPDVFQNGYPCQ 506
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
S71949
metalloproteinase 12 (EC 3.4.24.-) precursor - human
N;Alternate names: disintegrin 12; myeloma cell metalloproteinase MCMP
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 04-Feb-2000
C;Accession: S71949; PC4264
R;McKie, N.; Dallas, D.J.; Edwards, T.; Apperley, J.F.; Russell, R.G.G.; Croucher, P.I.
Biochem. J. 318, 459-462, 1996
A;Title: Cloning of a novel membrane-linked metalloproteinase from human myeloma cells.
A;Reference number: S71949; MUID:96404892; PMID:8809033
A;Accession: S71949
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-660 <MCK>
A;Experimental source: myeloma cells
R;McKie, N.; Edwards, T.; Dallas, D.J.; Houghton, A.; Stringer, B.; Graham, R.; Russell,
Biochem. Biophys. Res. Commun. 230, 335-339, 1997
A;Title: Expression of members of a novel membrane linked metalloproteinase family (ADAM
A;Reference number: PC4263; MUID:97168971; PMID:9016778
A;Accession: PC4264
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-337 <MCP>
A;Experimental source: articular chondrocyte
C;Function:
A;Description: involved in cell/cell and cell/matrix interaction in a variety of cell ty
A;Note: membrane-bound; belongs to repolysin family of metalloproteinases
C;Superfamily: mouse meltrin alpha; disintegrin homology
C;Keywords: hydrolase; metalloproteinase; zinc
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-660/Product: pre-metalloproteinase 12 #status predicted <MAT>
F;54-59/Region: autoinhibitory
F;295-378/Domain: disintegrin homology <DIS>
F;574-598/Region: epidermal growth factor-like
F;622-642/Domain: transmembrane #status predicted <TM1>
F;57,229,233,239/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;229,233,239/Binding site: zinc, catalytic (His) (active) #status predicted
F;230/Active site: Glu #status predicted

Query Match      49.8%; Score 306.5; DB 2; Length 660;
Best Local Similarity 49.5%; Pred. No. 9.4e-19;
Matches 48; Conservative 19; Mismatches 29; Indels 1; Gaps 1;

Qy 5 DIFNVKRCNGVVEGEECDGGLPKHKCAKDPCLL-SNCTLTGSGTCAFGLCCKDKCKFLPS 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 292 EAYSAPSGCNKLVDAAGECDGCTPKCELDPCCGSGTCKLSPFAECAYGDCCKDCRFLPG 351
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 64 GKVKRKEVNECDLPEWNCNGTSHKCPDDPFYVBDGIPCK 100
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 352 GTLCRGKTSECDVPCYCNSSQFCQPDVFQNGYPCQ 388
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
152361
testicular metalloproteinase-like, disintegrin-like, cysteine-rich protein IVa - crab-ea
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C;Accession: 152361
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R;Perry, A.C.F.; Jones, R.; Hall, L.
Biochem. J. 312, 239-244, 1995
A;Title: Analysis of transcripts encoding novel members of the mammalian metalloprotease-
active monkey tissues.
A;Reference number: I52361; MUID:96077150; PMID:7492319
A;Accession: I52361
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-732 <RES>
A;Cross-references: EMBL:X87205; NID:g1061158; PIDN:CAA60663.1; PID:g1061159
C;Genetics:
A;Gene: tMDC IVa
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;403-485/Domain: disintegrin homology <DIS>

Query Match      49.7%; Score 305.5; DB 2; Length 732;
Best Local Similarity 52.4%; Pred. No. 1.2e-18;
Matches 54; Conservative 10; Mismatches 38; Indels 1; Gaps 1;

Qy 1 VHTKDIENVKRCNGVVEGEECDGGLPKHKCAKDPCLL-SNCTLTGSGTCAFGLCCKDKCKF 60
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 397 VHNESITMV-RCGNLIVEGEECDGSGFKQCYASRCRSCRLTPGSGICHLDGDCCTNCSF 455
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 61 LPSSGKVKRKEVNECDLPEWNCNGTSHKCPDDPFYVBDGIPCKERG 103
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 456 SAQGTLCRPIQNICDLPEYCHGTITCPLDLYLQDGTPTCTEFG 498
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
S60257
meltrin alpha - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C;Accession: S60257
R;Yagami-Hiromasa, T.; Sato, T.; Kurisaki, T.; Kamiyo, K.; Nabeshima, Y.I.; Fujisawa-Sehara
Nature 377, 652-656, 1995
A;Title: A metalloproteinase-disintegrin participating in myoblast fusion.
A;Reference number: S60257; MUID:96026308; PMID:7566181
A;Accession: S60257
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-903 <VAG>
A;Cross-references: EMBL:D50411; NID:g1054586; PIDN:BAA08912.1; PID:g1054587
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;421-503/Domain: disintegrin homology <DIS>
F;349/Active site: Glu #status predicted

Query Match      47.8%; Score 294; DB 2; Length 903;
Best Local Similarity 49.5%; Pred. No. 1.3e-17;
Matches 48; Conservative 12; Mismatches 37; Indels 0; Gaps 0;

Qy 4 KDIFNVKRCNGVVEGEECDGGLPKHKCAKDPCLL-SNCTLTGSGTCAFGLCCKDKCKFLPS 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 417 KQAFGGRKCGVVEGEECDGCEPERCTNRCCNATTCTLKPDAVCAHGQCCDCQLKPP 476
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 64 GKVKRKEVNECDLPEWNCNGTSHKCPDDPFYVBDGIPCK 100
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 477 GTACRGSSNCDLPEFCFTGTPHCPANVYLHDGHPCCQ 513
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
I65253
disintegrin-like testicular metalloproteinase (EC 3.4.24.-) IVb - crab-eating macaque (f
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I65253
R;Perry, A.C.F.; Jones, R.; Hall, L.
Biochem. J. 312, 239-244, 1995
A;Title: Analysis of transcripts encoding novel members of the mammalian metalloprotease-
active monkey tissues.
A;Reference number: I52361; MUID:96077150; PMID:7492319
A;Accession: I65253
A;Status: preliminary; translated from GB/EMBL/DBJ
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 27, 2004, 22:08:28 ; Search time 23 Seconds  
(without alignments)  
233.184 Million cell updates/sec

Title: US-10-664-456-12\_COPY\_389\_491

Perfect score: 615

Sequence: 1 VHTKDFNVKRCNGVVEG.....SHKCPDDFYVEDGIPCKERG 103

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	615	100.0	820	1 AD29 HUMAN	Q9ukf5 homo sapien
2	446	72.5	726	1 AD20 HUMAN	Q43506 homo sapien
3	443	72.0	722	1 AD21 HUMAN	Q9ukj8 homo sapien
4	408	66.3	729	1 AD21 MOUSE	Q9ji76 mus musculus
5	404	65.7	760	1 AD25 MOUSE	Q9r159 mus musculus
6	382	62.1	697	1 AD26 MOUSE	Q9r158 mus musculus
7	357	58.0	790	1 AD30 HUMAN	Q9ukf2 homo sapien
8	351.5	57.2	761	1 AD24 MOUSE	Q9r160 mus musculus
9	314	51.1	920	1 AD19 MOUSE	Q35674 mus musculus
10	309	50.2	956	1 AD19 HUMAN	Q9h013 homo sapien
11	306.5	49.8	819	1 AD09 HUMAN	Q13443 homo sapien
12	294	47.8	903	1 AD12 MOUSE	Q61824 mus musculus
13	291.5	47.4	745	1 AD02 BOVIN	O77780 bos taurus
14	289	47.0	813	1 AD33 HUMAN	Q9bz11 homo sapien
15	283	46.0	909	1 AD12 HUMAN	Q43184 homo sapien
16	276.5	45.0	797	1 AD33 MOUSE	Q923w9 mus musculus
17	274	44.6	791	1 AD1A MOUSE	Q60813 mus musculus
18	273.5	44.5	935	1 AD22 XENLA	Q42596 xenopus lae
19	272	44.2	789	1 AD01 RAT	P70505 rattus norv
20	268.5	43.7	735	1 AD02 MOUSE	Q60718 mus musculus
21	265.5	43.2	857	1 AD22 MOUSE	Q9rlv6 mus musculus
22	264.5	43.0	906	1 AD22 HUMAN	Q9p0k1 homo sapien
23	263.5	42.8	735	1 AD02 HUMAN	Q99965 homo sapien
24	263.5	42.8	751	1 AD02 RABIT	Q28660 oryctolagus
25	263	42.8	824	1 AD08 HUMAN	P78325 homo sapien
26	262.5	42.7	737	1 AD08 RAT	Q63202 rattus norv
27	261.5	42.5	452	1 AD11 XENLA	Q9psz3 xenopus lae
28	261	42.4	735	1 AD02 CAVPO	Q60411 cavia porce
29	261	42.4	769	1 AD11 HUMAN	O75078 homo sapien
30	261	42.4	773	1 AD11 MOUSE	O9rlv4 mus musculus
31	260.5	42.4	735	1 AD02 MACFA	Q28478 macaca fasc
32	259	42.1	754	1 AD07 HUMAN	Q9h2u9 homo sapien
33	257	41.8	775	1 AD28 HUMAN	Q9ukq2 homo sapien

#### RESULT 1

ID	AD29 HUMAN	STANDARD;	PRT;	820 AA.
AC	Q9UKF5; Q9UHP1; Q9UKF3; Q9UKF4;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	ADAM 29 precursor (A disintegrin and metalloproteinase domain 29).			
GN	ADAM29.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).			
RC	TISSUE=Testis;			
RX	MEDLINE=99443746; PubMed=10512762;			
RA	Carratti D.P., DuBose R.F., Black R.A., Nelson N.;			
RT	"Isolation of two novel metalloproteinase-disintegrin (ADAM) cDNAs			
RT	that show testis-specific gene expression.";			
RL	Biochem. Biophys. Res. Commun. 263:810-815(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RC	TISSUE=Testis;			
RX	MEDLINE=20112771; PubMed=10644455;			
RA	Xu R., Cai J., Xu T., Zhou W., Ying B., Deng K., Zhao S., Li C.;			
RT	"Molecular cloning and mapping of a novel ADAM gene (ADAM29) to human			
RT	chromosome 4.";			
RL	Genomics 62:537-539(1999).			
CC	-I- FUNCTION: May be involved in spermatogenesis and fertilization.			
CC	Seems to be a non catalytic metalloprotease-like protein.			
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-I- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=3;			
CC	Names=Alpha;			
CC	IsoId=Q9UKF5-1; Sequence=Displayed;			
CC	Names=Beta;			
CC	IsoId=Q9UKF5-2; Sequence=VSP_005491;			
CC	Names=Gamma;			
CC	IsoId=Q9UKF5-3; Sequence=VSP_005492, VSP_005493;			
CC	TISSUE SPECIFICITY: Expressed specifically in testes.			
CC	-I- SIMILARITY: Contains 1 EGF-like domain.			
CC	-I- SIMILARITY: Contains 1 disintegrin domain.			
CC	-I- SIMILARITY: Belongs to peptidase family M12B.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announcement/">http://www.isb-sib.ch/announcement/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; AF171929; AAF03777.1; -			
DR	EMBL; AF171930; AAF03778.1; -			
DR	EMBL; AF171931; AAF03779.1; -			

Q28475 macaca fasc  
Q05910 mus musculu  
Q9x816 macaca fasc  
Q8r534 mus musculu  
Q63180 rattus norv  
Q35227 mus musculu  
P30431 bothrops ja  
O13766 schistosacch  
Q13444 homo sapien  
Q88839 mus musculu  
Q9gyv0 x adam 15 p  
Q9jln6 mus musculu

#### ALIGNMENTS





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 27, 2004, 22:11:58 ; Search time 33 Seconds  
(without alignments)  
161.136 Million cell updates/sec

Title: US-10-664-456-12\_COPY\_389\_491  
Perfect score: 615  
Sequence: 1 VHTKDIENVRKCGVVEEG.....SHKCPDDFYVEDGIPCKERG 103

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	443	72.0	722	4	US-09-617-145-2
2	309	50.2	751	2	US-08-836-443-3
3	289	47.0	746	4	US-09-548-797B-4
4	289	47.0	787	4	US-09-548-797B-5
5	289	47.0	802	4	US-09-632-098-2
6	289	47.0	812	4	US-09-632-098-4
7	289	47.0	849	4	US-09-548-797B-6
8	268.5	43.7	457	1	US-08-264-101-4
9	268.5	43.7	457	2	US-08-765-243-4
10	268.5	43.7	457	5	PCT-US95-07295-4
11	268.5	43.7	735	2	US-08-765-243-6
12	268.5	43.7	735	5	PCT-US95-07295-6
13	263.5	42.8	651	1	US-08-264-101-2
14	263.5	42.8	651	2	US-08-765-243-2
15	263.5	42.8	651	5	PCT-US95-07295-2
16	263.5	42.8	734	2	US-08-765-243-8
17	263.5	42.8	734	5	PCT-US95-07295-8
18	261	42.4	488	1	US-08-243-542-1
19	261	42.4	488	1	US-08-477-407-1
20	261	42.4	488	1	US-08-484-355-1
21	261	42.4	524	1	US-08-243-542-2
22	261	42.4	524	1	US-08-477-407-2
23	261	42.4	524	1	US-08-484-355-2
24	261	42.4	670	1	US-08-243-542-3
25	261	42.4	670	1	US-08-477-407-3
26	261	42.4	670	1	US-08-484-355-3
27	261	42.4	769	1	US-08-243-542-4

28	261	42.4	769	1	US-08-477-407-4	Sequence 4, Appli
29	261	42.4	769	1	US-08-484-355-4	Sequence 4, Appli
30	257	41.8	540	4	US-09-786-256C-1	Sequence 1, Appli
31	257	41.8	540	4	US-09-786-256C-30	Sequence 15, Appl
32	257	41.8	775	4	US-09-786-256C-15	Sequence 30, Appl
33	257	41.8	775	4	US-09-786-256C-32	Sequence 32, Appl
34	245.5	39.9	814	3	US-09-813-819-4	Sequence 4, Appli
35	245.5	39.9	814	4	US-09-920-048-4	Sequence 4, Appli
36	245.5	39.9	855	3	US-09-813-819-2	Sequence 2, Appli
37	245.5	39.9	855	4	US-09-920-048-2	Sequence 2, Appli
38	241	39.2	96	4	US-09-786-256C-2	Sequence 2, Appli
39	241	39.2	696	3	US-09-351-414-2	Sequence 2, Appli
40	239	38.9	529	2	US-08-836-442-3	Sequence 3, Appli
41	237	38.5	621	4	US-09-026-001A-6	Sequence 6, Appli
42	235.5	38.3	781	4	US-09-738-946-8	Sequence 8, Appli
43	232	37.7	613	4	US-09-026-001A-10	Sequence 10, Appl
44	232	37.7	621	4	US-09-026-001A-18	Sequence 18, Appl
45	229	37.2	616	4	US-09-608-790-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-09-617-145-2  
; Sequence 2, Application US/09617145  
; Patent No. 6485956  
; GENERAL INFORMATION:  
; APPLICANT: Cerretti, Douglas P.  
; TITLE OF INVENTION: SVPHI-8 DNA and Polypeptides  
; FILE REFERENCE: 03260.0050-00304  
; CURRENT APPLICATION NUMBER: US/09/617.145  
; CURRENT FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/071.505  
; PRIOR FILING DATE: 1998-01-14  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 722  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-617-145-2

Query Match	72.0%	Score 443;	DB 4;	Length 722;
Best Local Similarity	71.1%	Pred. No. 4.1e-32;		
Matches	69;	Conservative	15;	Mismatches 13; Indels 0; Gaps 0;
Qy	5	DIFNVKCGNGVVEEGECDCGPKLKHCAKDCCLSNCTLTGSTCAFLGCKCKFKLPSG	64	
Db	402	EIFMLKRCNGVVEREEQCDCGVSQCEQDACCLLNLCTLRFGAACAFGLCKCKCKFKMPSPG	461	
Qy	65	KVCRKEVNECDLPWCNGTSHKCPDDFYVEDGIPCKE	101	
Db	462	ELCRQEVNECDLPWCNGTSHQCPEDRYVQDGI PCSD	498	
RESULT 2				
US-08-836-443-3				
; Sequence 3, Application US/08836443				
; Patent No. 5883241				
; GENERAL INFORMATION:				
; APPLICANT: DOCHERTY, Andrew, J.P				
; APPLICANT: SLOCOMBE, Patrick, M.				
; TITLE OF INVENTION: DNA SEQUENCES CODING FOR A				
; NUMBER OF SEQUENCES: 4				
; CORRESPONDENCE ADDRESS:				
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP.				
; STREET: 130 Water Street				
; CITY: Boston				
; STATE: MA				
; COUNTRY: USA				
; ZIP: 02109				

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,443
; FILING DATE: 01-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9709420
; FILING DATE: 05-SEP-1997
; APPLICATION NUMBER: 9612145.4
; FILING DATE: 11-JUN-1996
; APPLICATION NUMBER: 9526230.9
; FILING DATE: 21-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 47424
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5883241e
; US-08-836-443-3

Query Match 50.2%; Score 309; DB 2; Length 751;
Best Local Similarity 51.5%; Pred. No. 3.9e-20;
Matches 51; Conservative 16; Mismatches 30; Indels 2; Gaps 2;

Qy 3 TKDIFNVKRCGVVEGEEDCGPLKHCADPCC-LSNCTLTGSGTCFAFLCKCKFL 61
Db 235 TRMVGGRRCGVLEGEEDCGEEEC-NNPCNASNCTLRPGAECAGHSCCHQCKLL 293

Qy 62 PSGVKRKEVNECDLPWCNGTSHKCPDDFYVEDGIPCK 100
Db 294 APGTLCEARQCDDLPFCSTKSPCHPTNFQMDGTCE 332

RESULT 3
US-09-548-797B-4
; Sequence 4, Application US/09548797B
; Patent No. 6683165
; GENERAL INFORMATION:
; APPLICANT: KEITH, TIM
; TITLE OF INVENTION: NOVEL HUMAN GENE RELATING TO RESPIRATORY DISEASES AND
; FILE REFERENCE: 2976-4039
; CURRENT APPLICATION NUMBER: US/09/548,797B
; CURRENT FILING DATE: 2002-11-26
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 746
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-548-797B-4

Query Match 47.0%; Score 289; DB 4; Length 746;
Best Local Similarity 55.1%; Pred. No. 2.4e-18;
Matches 49; Conservative 12; Mismatches 26; Indels 2; Gaps 2;

Qy 12 CGNGVVEGEEDCGPLKHCADPCCLS-NCTLTGSGTCFAFLCKCKFLPSGKVCCKE 70
Db 479 MGCDDLPEFCTGTSSHCPCPDVYLLDGSPC 507

US-09-632-098-2
; Sequence 2, Application US/09632098
; Patent No. 6420154
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
; FILE REFERENCE: 99-39
; CURRENT APPLICATION NUMBER: US/09/632,098
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-632-098-2

Query Match 47.0%; Score 289; DB 4; Length 802;
Best Local Similarity 55.1%; Pred. No. 2.5e-18;
Matches 49; Conservative 12; Mismatches 26; Indels 2; Gaps 2;

Qy 12 CGNGVVEGEEDCGPLKHCADPCCLS-NCTLTGSGTCFAFLCKCKFLPSGKVCCKE 70
Db 420 CGNGFVEAGEEDCGPGQEC-RDLCFFAHNCSLRPGAQCAHGDCVCRLLKPAGALCRQA 478

Qy 71 VNECDLPWCNGTSHKCPDDFYVEDGIPC 99
Db 479 MGCDDLPEFCTGTSSHCPCPDVYLLDGSPC 507

US-09-548-797B-5
; Sequence 5, Application US/09548797B
; Patent No. 6683165
; GENERAL INFORMATION:
; APPLICANT: KEITH, TIM
; TITLE OF INVENTION: NOVEL HUMAN GENE RELATING TO RESPIRATORY DISEASES AND
; FILE REFERENCE: 2976-4039
; CURRENT APPLICATION NUMBER: US/09/548,797B
; CURRENT FILING DATE: 2002-11-26
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-548-797B-5

Query Match 47.0%; Score 289; DB 4; Length 787;
Best Local Similarity 55.1%; Pred. No. 2.5e-18;
Matches 49; Conservative 12; Mismatches 26; Indels 2; Gaps 2;

Qy 12 CGNGVVEGEEDCGPLKHCADPCCLS-NCTLTGSGTCFAFLCKCKFLPSGKVCCKE 70
Db 420 CGNGFVEAGEEDCGPGQEC-RDLCFFAHNCSLRPGAQCAHGDCVCRLLKPAGALCRQA 478

Qy 71 VNECDLPWCNGTSHKCPDDFYVEDGIPC 99
Db 479 MGCDDLPEFCTGTSSHCPCPDVYLLDGSPC 507

US-09-632-098-2
; Sequence 2, Application US/09632098
; Patent No. 6420154
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
; FILE REFERENCE: 99-39
; CURRENT APPLICATION NUMBER: US/09/632,098
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-632-098-2

Query Match 47.0%; Score 289; DB 4; Length 802;
Best Local Similarity 55.1%; Pred. No. 2.5e-18;
Matches 49; Conservative 12; Mismatches 26; Indels 2; Gaps 2;

Qy 12 CGNGVVEGEEDCGPLKHCADPCCLS-NCTLTGSGTCFAFLCKCKFLPSGKVCCKE 70
Db 420 CGNGFVEAGEEDCGPGQEC-RDLCFFAHNCSLRPGAQCAHGDCVCRLLKPAGALCRQA 478

Qy 71 VNECDLPWCNGTSHKCPDDFYVEDGIPC 99
Db 479 MGCDDLPEFCTGTSSHCPCPDVYLLDGSPC 507
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 27, 2004, 22:01:22 ; Search time 116 Seconds  
(without alignments)  
280.158 Million cell updates/sec

Title: US-10-664-456-12\_COPY\_389\_491

Perfect score: 615

Sequence: 1 VHTKDFNVKRCGVVEG.....SHKCPDDFYVEDGIPCKERG 103

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	449	73.0	763	11 Q811Q4	Q811Q4 mus musculus
2	386	62.8	697	11 Q8BMR4	Q8BMR4 mus musculus
3	382	62.1	702	11 Q8BMR5	Q8BMR5 mus musculus
4	382	62.1	714	11 Q8K4K0	Q8K4K0 mus musculus
5	357	58.0	790	4 Q8T8Z7	Q8T8Z7 homo sapien
6	353.5	57.5	761	11 Q8CDV3	Q8CDV3 mus musculus
7	340	55.3	732	11 Q811Q3	Q811Q3 mus musculus
8	325	52.8	703	11 P97777	P97777 rattus norv
9	316.5	51.5	845	11 Q61072	Q61072 mus musculus
10	316.5	51.5	853	11 Q80U94	Q80U94 mus musculus
11	314	51.1	473	11 Q60815	Q60815 mus musculus
12	314	51.1	763	11 Q8CGQ2	Q8CGQ2 mus musculus
13	312	50.7	703	11 Q8C0V3	Q8C0V3 mus musculus
14	311	50.6	730	6 O19051	O19051 oryctolagus
15	307.5	50.0	873	13 O42595	O42595 xenopus lae
16	306.5	49.8	655	4 Q8NFM6	Q8NFM6 homo sapien

17	305.5	49.7	732	6 Q28484	Q28484 macaca fasc
18	304	49.4	731	6 O19050	O19050 oryctolagus
19	303	49.3	754	11 Q8CGQ1	Q8CGQ1 mus musculus
20	298.5	48.5	735	6 Q866A8	Q866A8 sus scrofa
21	298	48.5	751	11 P70535	P70535 rattus norv
22	293	47.6	713	6 Q28485	Q28485 macaca fasc
23	289	47.0	474	6 Q95LW7	Q95LW7 macaca fasc
24	289	47.0	735	11 Q60473	Q60473 cavia porce
25	289	47.0	812	4 Q8N0W6	Q8N0W6 homo sapien
26	289	47.0	919	6 Q28659	Q28659 oryctolagus
27	284	46.2	914	13 O12960	O12960 xenopus lae
28	282	45.9	825	6 Q28477	Q28477 macaca fasc
29	282	45.9	838	6 O19056	O19056 papio anubi
30	282	45.9	899	13 Q8UVF1	Q8UVF1 coturnix co
31	282	45.9	905	6 Q28476	Q28476 macaca fasc
32	281	45.7	825	6 O46652	O46652 papio anubi
33	280	45.5	792	6 O19061	O19061 saguinus oe
34	280	45.5	804	11 Q60410	Q60410 cavia porce
35	276.5	45.0	797	11 Q8R465	Q8R465 mus musculus
36	276.5	45.0	797	11 Q8R5G5	Q8R5G5 mus musculus
37	273.5	44.5	706	13 Q42593	Q42593 xenopus lae
38	273	44.4	612	13 Q7T046	Q7T046 vipera lebe
39	272	44.2	697	13 Q72Y29	Q72Y29 brachydanio
40	271	44.1	1023	5 Q967H9	Q967H9 strongyloce
41	265.5	43.2	694	5 Q9GZ15	Q9GZ15 drosophila
42	265.5	43.2	1182	5 Q9VXL1	Q9VXL1 drosophila
43	265	43.1	821	6 O19060	O19060 saguinus oe
44	265	43.1	836	6 O19057	O19057 ponga pygma
45	264	42.9	612	13 Q8UVG0	Q8UVG0 bothrops er

#### ALIGNMENTS

RESULT 1

Q811Q4 ID Q811Q4 PRELIMINARY; PRT; 763 AA.  
AC Q811Q4;  
DT 01-JUN-2003 (Tremblrel. 24, Created)  
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE ADAM29.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]\_TaxID=10090;  
RP SEQUENCE FROM N.A.  
RC STRAIN=ICR; TISSUE=Testis;  
RA Choi I., Cho C.;  
RT "Cloning and characterization of ADAM29.";  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY190759; RA038663.1; -  
DR GO; GO:0004224; F:metalloendopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR006586; ADAM\_cysteine.  
DR InterPro; IPR001762; Disintegrin.  
DR InterPro; IPR001590; Peptidase\_M12B.  
DR InterPro; IPR002870; Peptidase\_M12B\_N.  
DR Pfam; PF00200; disintegrin; 1.  
DR Pfam; PF01562; Pep\_M12B\_propep; 1.  
DR Pfam; PF01421; Reprolysin; 1.  
DR PRINTS; PR00289; DISINTEGRIN.  
DR ProDom; PD000664; Disintegrin; 1.  
DR SMART; SM00608; ACR; 1.  
DR SMART; SM00050; DISIN; 1.  
DR PROSITE; PS00215; ADAM\_MEPRO; 1.  
DR PROSITE; PS00427; DISINTEGRIN\_1; 1.  
DR PROSITE; PS00214; DISINTEGRIN\_2; 1.  
SQ SEQUENCE 763 AA; 86444 MW; F9EF082C3BFBA80 CRC64;

Query Match 73.0%; Score 449; DB 11; Length 763;  
Best Local Similarity 72.7%; Pred. No. 2.5e-45;

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Matches 72; Conservative 14; Mismatches 13; Indels 0; Gaps 0;
QY 1 VHTKIDFNVKCGVVEGECDCGPLKHKAKDPCLSNCTLTGSTCAFGLCCKCKP 60
   :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 395 MYTKDIFDTRCGVVEGECDCGSLRNCTNDLCCMSNCTLTGSSCAFGLCCKNQF 454
   ||||:|:| | |||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
QY 61 LPSGKVCKEVNECDLPENCNCTSHKCPDDFYVEDGIPC 99
   ||||:|:| | |||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 455 LPSGTLCKRDNICDLPENCNCTSHKCPDDFYVEDGIPC 493
   ||||:|:| | |||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||

RESULT 2
Q8BMR4 ID Q8BMR4 PRELIMINARY; PRT; 697 AA.
AC Q8BMR4;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DE Similar to ADAM 26 precursor.
GN ADAM26.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
   60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK029590; BAC26524.1; -.
DR MGD; MGI:2181992; Adam34.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0008270; P:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS0215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS0214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 697 AA; 78760 MW; E917E7E88B7F57E7 CRC64;

Query Match 62.8%; Score 386; DB 11; Length 697;
Best Local Similarity 64.3%; Pred. No. 8.3e-38;
Matches 63; Conservative 11; Mismatches 24; Indels 0; Gaps 0;
QY 6 IFNVKCGVVEGECDCGPLKHKAKDPCLSNCTLTGSTCAFGLCCKCKP 65
   :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 389 VTNLTVCGNKVVVEGECDCGNSCLQDPCSSDCVLKPGAQCAFGLCCKNQFLKAGT 448
   ||||:|:| | |||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
QY 66 VCRKEVNECDLPENCNCTSHKCPDDFYVEDGIPCKERG 103
   ||||:|:| | |||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 449 VCRKEKNECDLPENCNCTSHKCPDDFYVEDGIPCKERG 486
   ||||:|:| | |||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||

RESULT 3
Q8BMR5 ID Q8BMR5 PRELIMINARY; PRT; 702 AA.
AC Q8BMR5;
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DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DE Similar to ADAM 26 precursor.
GN ADAM34.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
   60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK029590; BAC26524.1; -.
DR MGD; MGI:2181992; Adam34.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0008270; P:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS0215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS0214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 702 AA; 79278 MW; 31976863CA4C80EE CRC64;

Query Match 62.1%; Score 382; DB 11; Length 702;
Best Local Similarity 66.3%; Pred. No. 2.5e-37;
Matches 61; Conservative 10; Mismatches 21; Indels 0; Gaps 0;
QY 12 CGNGVVEGECDCGPLKHKAKDPCLSNCTLTGSTCAFGLCCKCKP 71
   ||||:|:| | |||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 398 CGNVLVEGECDCGSTESCLQDPCSSDCVLKPGAQCAFGLCCKNQFLKGTVCREEK 457
   ||||:|:| | |||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
QY 72 NECDLPENCNCTSHKCPDDFYVEDGIPCKERG 103
   ||||:|:| | |||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 458 NECDLPENCNCTSHKCPDDFYVEDGIPCKERG 489
   ||||:|:| | |||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||

RESULT 4
Q8K4K0 ID Q8K4K0 PRELIMINARY; PRT; 714 AA.
AC Q8K4K0;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE Testase 4.
GN ADAM34.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=22030469; PubMed=12034510;
RA Brachvogel B., Reichenberg D., Beyer S., Jehn B., von der Mark K.,
RA Bieleke W.;
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